

AMENDMENTS TO THE SPECIFICATION

Please replace paragraph on **page 39, lines 3-9** with the following amended paragraph:

Similar methods were used for analysis of microsatellite markers in the brachymorphic mice, using DNA samples from backcross animals recombinant in the *bm* region. (Rusiniak, M.E., et al., *Molecular markers near the mouse brachymorphic (bm) gene, which affects connective tissues and bleeding time*, Mamm. Genome 7:98-102 [1996]). Markers were derived from the Whitehead Institute for Biomedical Research mouse genetic and physical mapping database (<http://www-genome.wi.mit.edu/cgi-bin/mouse/index>).

Please replace paragraph on **page 40, lines 1-6** with the following amended paragraph:

Radiation Hybrid Mapping. DNA from the Genebridge 4 Radiation Hybrid (RH) panel was obtained from Research Genetics. For the *PAPSS2* gene, a 236 bp PCR product was amplified using primers 5'- CTGGTGCTGGAAAAACAACG-3' (SEQ. ID. NO.:5; forward primer) and 5'- TGCGAATGGAGAA ATAAAGCTG-3' (SEQ. ID. NO.:6; reverse primer). RH data were submitted to the Whitehead server (<http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl>) for placement on the RH map.

Please replace paragraph on **page 40, lines 7-14** with the following amended paragraph:

Computer Methods. BLAST searches (Altschul, S.F., et al., *Gapped BLAST and PSI-BLAST: a new generation of protein search programs*, Nucleic Acids Res. 25:3389-3402 [1997]) and determinations of sequence homology were performed using the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/BLAST/>) and Baylor College of Medicine (http://dot.imgen.bcm.tmc.edu:9331/seq-search/nucleic_acid-search.html) servers. The phenotypic map of the mouse genome was accessed through the Mouse Genome Informatics server (<http://www.informatics.jax.org>), maintained by the Jackson Laboratory.